

QY	346	AAVALAASGIVASNNI	LEETPRVALVAGVGYTYTMEP	PHASNNISERAPTY	366
Db	1035	TGCGTCAATGGAACAC	TTATGCGGGTGTGGAGGATATATGTTCAACCACTCAATTA	109	
QY	366	IAENMETVALLEUALATY	TAENPLEUALASERAGTUTPRLEUPROLEUASNAHGERYA	386	
Db	1095	TAAACATGGTCTAGCGGATATACCTTGCTCTTAGAGAGTGGCTTCCATTAACCGTTCCT	115		
QY	386	IAENASNAVALVALATGTYTGLYHISERLEUALALEUTYLVASAPLYILETYTWE	406		
Db	1155	GAACAAATGCGTGTGTTAGATATAGTCAATCTTGGCATTAATCAAGGATTAATAATTACAT	121		
QY	406	LYTGTGLYGLYLVLEI	ASAPRO-THGIVASNVATHRASNGILEUATGVALPHENISI	426	
Db	1215	GTATGGAGGAAAAATTGATTTC-AACTGGAAATGTGACCAATAGTTGAGACGTTTTCACA	1273		
QY	426	LEHIASNGIUSERTPVALLEULEUTHPRLOYALALAYGLINGINTYRALVALVALG	446		
Db	1274	TTCAATATGACATACAGCGGTGTGTGGACCCCTTAAGCAAAAGACAGATATGCAGGTGG	1333		
Db	446	LYHISERALAHISILEVALTHLEULYASNGIVARVALVAMETLEUVALIIEPHG	466		
Db	1334	GGCACTCTGCACACATTGTTTACCTGAAOMATGCCCAAGTGCATGCTGATCTTGG	1393		
QY	466	LYHISCYPROLEUTYTGLYTYTII	ESERASNAVLINGIULTYASPLEUASPLYSANT	486	
Db	1394	GTCACTGCCCTCTCATGATATATATACCAATGTGTCAGAAATATGATTTGGATTAAGAAC	1453		
QY	486	HRTTSEIILEUENITHRNGIUYALALEUVALINGIULYTYTGLYHISERSERV	506		
Db	1454	CATGAGATATATACACACCCAGGTGCCCTTGTGCAAGGGGGTATAGCGGCATATGCAGTG	1513		
QY	506	ALLTYRAPHISARSTHARGLALEUTYVALHISGLYLYTYRLEUALAPHESERILAA	526		
Db	1514	TTTACGACCAATAGACACAGGGCCCTATACGTTACGTTAGGTGCTACAAGGCTTCACTGCCA	1573		
QY	526	SNLYSTYRATGLEUALASAPRPLEUTYRATGTYTASAPVALAPRTHGLMETTPRHT	546		
Db	1574	ATTAAGTACCGGCTTGCAAGATATCTTACCGATATGATGGAATACCAATATGGACCA	1633		
QY	546	LELEULYASPSERARSPHEPHEARGTYRLEUENITHRALVALIILEVALSERGLYTHRM	566		
Db	1634	TTCTTAAAGCACAGCGCAATTTTCCGTTACTTGACACAGCTGTGATATGATAGGAAACCA	1693		
QY	566	ETLEUVALPHEGIVGLYASANTHNIASASAPRTHSERMETSERHISGLYALALYSCYAP	586		
Db	1694	TGCTGTGTTTGGGGAAACACACACATATACATCTATAGCAGCATGGGCCAAATGTCT	1753		
Db	586	HESESERAPRPHMETALATYRASPRIILEIACYSASAPATGTPSERVALLEUPROARAP	606		
Db	1754	TTCCTTCAGATTTCAATGCTTATGACATTCCTCTGTGACCGCTGTGATAGTGTCCAGAC	1813		
QY	606	TOASPRLEUENIHISASAPVALASAPRPHNEGLYHISERILAVALLEUENISASERTHRM	626		
Db	1814	CTGATCTCCACCAATGATGTCAACAGATTTGGCCATTCAGACAGTCTTACACACAGACACA	1873		
QY	626	ETTYRVALPHEGIVGLYPHENASERLEUENUSERAPRIILEUVALPHETHRSERG	646		
Db	1874	TGATATGTTCCGTGTTTCAATATGCTCTCTCTCAAGCAACATCTCGATATACCTCGG	1933		
QY	646	INGIUCYASAPALAHISARSGERGLUALALACYSEULALALAGIYPROGYIILEATYGC	666		
Db	1934	AACAGGTATATGCGCATCCGAGGAAAGCGCTTGTTTACACAGGACCTGATATTCGAT	1993		
QY	666	YVALTTPRANRTHGISYERSEGINCYIILASERTTPALALEUALATHRAPGJUNG	686		
Db	1994	GTGTGTGACACAGGATGCTCTCAGTATCTCGTGGCGCTGCAACTGTATGAACAG	2053		
QY	686	INGIULYSEULYSSERGICYSPHESERTLYSARSTHLEUASPHISASAPRACYASAPG	706		
Db	2054	AAGAAAGATTAAATACAGATATGTTTTTCCAAAGAACCTTTGACATATACATAGATGTGCC	2113		

[illegible]

	RESULT	8
	ABO111120	
LOCUS	ABO111120	
DEFINITION	Homo sapiens mRNA for KIAA0548 protein, partial cds.	PRI 10-APR-1999
ACCESSION	ABO111120	
VERSION	ABO111120.1	GI:3043619
KEYWORDS	KIAA0548 protein.	
SOURCE	Homo sapiens male brain cDNA to mRNA, clone JH-0318ec; submitted by	

BASE COUNT	1535 a	1505 c	1269 g	1523 t
ORIGIN				
Alignment Scores:				
Pred. No.:	0			
Length:				5633

Score: 452.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 31.63%
DB: 9
Matches: 452
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-787-097-12 (1-1429) x AB011120 (1-5632)

Qy 978 ThrmSerThrCysProProGluAsnGlySerGlyThrCysThrCysSerHisGlyLeu 997
Db 3 AGCATGACACCTGCCCCCTGAAAATTGTTCAAGCTACTGTAATCTGATCTGCTTGG 62
Qy 998 GluGlnProCysGlyGlyTyrCysThrAspProSeranthrglyGlyGlyCysile 1017
Db 63 GAGCAACGAGCTGTGCTGTGTAATGATCCCGAAGTACTGCAAGGAAATGCAAT 122
Qy 1018 GluGlySerTyrGlyGlyProValLysMetProSerGlnAlaProthrglyAsnPhetYr 1037
Db 123 GAGGTTCTTAAGAACCAAGTAAAGATGCTTCCGACCCCTTACAGGAAATTTCTAT 182
Qy 1038 ProGlnProLeuLeuAsnSerSerMetCysLeuGluAspSerArgTyrAsnTrpSerPhe 1057
Db 183 CCAAGCCCTGCTCAATTCAGCATGTGCTAGAGGACAGCATACCACTGCTTTC 242
Qy 1058 IleHisCysProAlaCysGlnCysAsnGlyHisSerLysCysIleAsnGlnSerIleCys 1077
Db 243 ATTCACGTGTCAGCTTCCCATATGACAGCCACAGTAATGATCATACAGCATCTGT 302
Qy 1078 GluLysCysGluAsnLeuThrThrglyLysHisCysGlyLysIleSerGlyPheTyr 1097
Db 303 GAAAGCTGTGAGAACCTGACACAGGCAAGCACTGAGAACCTGCAATTCGCTTAC 362
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Db 363 GGTGATCCCAACCAATGAGGAAATGTCAGCATGCAAGTCAATGAGGCAAGCTCTG 422
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Db 483 CAGCTATGTGAGGTAAGAAATGATGATCAAGAAACCTCTCAAGAGAAACATGTTATAT 542
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Qy 1298 AlaValValTyrLysIleLysGlnSerCysTrpAlaSerArgArgGluGlnLeu 1317

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Db 1023 CGAAGATGCAACAGATGCGCACCTCTTGGCTCTCTGTAATGTCCTTGAACA 1082
Qy 1338 AspGluGlnProPhePheIleGlyGlySerIleLysThrValProLysProIleAla 1357
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Qy 1358 LeuGlnProCysPheGlyAsnLysAlaValLysSerValPheValArgLeuProArg 1377
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Qy 1378 GlyLeuGlyGlyIleProProProGlyGlnSerGlyLeuAlaValAlaSerAlaLeuVal 1397
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Qy 1398 AspIleSerGlnGlnMetProIleValTyrLysGlyLysSerGlyAlaValArgAsnArg 1417
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Qy 1418 LysGlnGlnProProAlaGlnProGlyThrCysIle 1429
Db 1323 AAGCAGACAGCCCCCTGACAGCTGCGAGCTGCACTC 1358

RESULT 9
AF531101
LOCUS
DEFINITION Bos taurus attractin mRNA, complete cds.
ACCESSION AF531101
VERSION AF531101.1 GI:22297307
KEYWORDS
SOURCE
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 493)
Graphodatskaya, D., Joerg, H. and Stranzinger, G.
TITLE
Direct Submision
JOURNAL
Submitted (18-JUL-2002) Animal Sciences, ETH, Tannenstrasse 1,
Zurich, CH 8092, Switzerland
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